This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Sharpe, Sharpe
Borriello, Francescopaolo
Freeman, Gordon
Nadler, Lee

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules and Uses Therefor

(iii) NUMBER OF SEQUENCES: 65

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 28 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/205,697
(B) FILING DATE: 02-Mar-1994

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Mandragouras, Amy E.
(B) REGISTRATION NUMBER: 36,207
(C) REFERENCE/DOCKET NUMBER: BWI-120CPUS

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (617)227-7400
(B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1888 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 249..1208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC      60

TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG     120

TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA     180

GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT     240

CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC       290
         Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
           1               5                  10

AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT       338
Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg
 15                  20                  25                  30

CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG       386
Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val
                 35                  40                  45

AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT       434
Lys Asp Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp
             50                  55                  60

GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG       482
Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu
         65                  70                  75

TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG       530
Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg
     80                  85                  90

ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC       578
Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val
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100    95                  100                 105                 110
101
102   CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA       626
103   Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg
104                   115                 120                 125
105
106   GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA       674
107   Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys
108               130                 135                 140
109
110
111   GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG TCT GGA AAC CCA TCT GCA       722
112   Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala
113           145                 150                 155
114
115   GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC GGG GGT TTC CCA AAG CCT       770
116   Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro
117       160                 165                 170
118
119   CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG       818
120   Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr
121   175                 180                 185                 190
122
123   ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA       866
124   Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln
125                   195                 200                 205
126
127   CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA       914
128   Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys
129               210                 215                 220
130
131   TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA       962
132   Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro
133           225                 230                 235
134
135   GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA      1010
136   Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
137       240                 245                 250
138
139   TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC ATC AAA TGC      1058
140   Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
141   255                 260                 265                 270
142
143   TTC TGT AAG CAC GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA      1106
144   Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala
145                   275                 280                 285
146
147   AAG GAC TTC AGA AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT      1154
148   Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
149               290                 295                 300
150
151   CTA GGT GAA GCC TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA      1202
152   Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu
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153          305                 310                 315
154
155  CCA CAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA       1258
156  Pro Gln
157      320
158
159  GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACAC ACACACACAC    1318
160
161  ACACACACAC ACACACACAC ACACACACAC ACACACACAC TCTCTCTCTC TCTCTCTCTC    1378
162
163  GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA    1438
164
165  GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG    1498
166
167  GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA    1558
168
169  GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA    1618
170
171  ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT    1678
172
173  TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA    1738
174
175  CTAGCCTCTA TTTTGTTTGT TTTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA    1798
176
177  CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC    1858
178
179  TTTCCAGGTA TTTCCCTTTT TATCCTTCAT                                     1888
180
181
182  (2) INFORMATION FOR SEQ ID NO:2:
183
184         (i) SEQUENCE CHARACTERISTICS:
185               (A) LENGTH: 320 amino acids
186               (B) TYPE: amino acid
187               (D) TOPOLOGY: linear
188
189        (ii) MOLECULE TYPE: protein
190
191        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
192
193  Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
194    1               5                  10                  15
195
196  Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
197                20                  25                  30
198
199  Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
200           35                  40                  45
201
202  Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
203       50                  55                  60
204
205  Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
```

65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
85 90 95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
100 105 110

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp
130 135 140

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr
145 150 155 160

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
165 170 175

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
180 185 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp
195 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly
210 215 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys
260 265 270

Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp
275 280 285

Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly
290 295 300

Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2516 base pairs

****** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 226 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
 1               5                  10                  15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser
            20                  25                  30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
        35                  40                  45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser
    50                  55                  60

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val
65                  70                  75                  80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
                85                  90                  95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser
            100                 105                 110

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
        115                 120                 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Pro Pro
    130                 135                 140

Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
145                 150                 155                 160

Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys
                165                 170                 175

Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala
            180                 185                 190
```

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3048   Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
3049            195                 200                 205
3050
3051   Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu
3052       210                 215                 220
3053
3054   Pro Gln
3055   225
3056
3057
3058
3059
3060
3061
3062
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/702,525*

DATE: 01/12/98
TIME: 12:00:40

INPUT SET: S22465.raw

Line	Error	Original Text